IN THE CLAIMS

Delete claims 6-7; 9-25.

8. (AMENDED) A [computer system] method for quantitating [determining] the viral load, if any, found within samples applied to a microarray [effect of one or more therapies upon a subject] comprising [a processor and a memory coupled to said processor, said memory encoding one or more programs, said one or more programs causing said processor to perform] the following steps:

[generating a viral diffusion curve based on known viral load studies associated with the therapy of interest;]

identifying hybridization activity from an output pattern from at least two samples applied to at least one microarray;

[calibrating the] generating a viral diffusion curve [based on] using at least two viral load measurements based on the identified hybridization activity;

mapping [each of] the identified hybridization activity to coordinates on the viral diffusion curve [output patterns representative of hybridization activity to respective coordinates]; and

quantitating [determining] the viral load by interpreting the coordinates of the [calibrated] viral diffusion curve.

Please add new claims 26-33.

26. The method of claim 8 wherein the mapping step generates an iterated fractal system to map the hybridization activity onto the viral diffusion curve.

27. The method of claim 8 wherein the generation step employs nonlinear information filtering to generate the viral diffusion curve.

29. The method of claim 8 further including the step of determining whether a therapy of interest has been effective based upon the degree of convergence from one sample to another.

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30. The method of claim 8 wherein the viral diffusion curve is generated by populating a Fokker-Planck equation with the viral load measurements.

31. The method of claim 8 wherein the Fokker-Planck equation utilized to generate the viral diffusion curve is dependent upon the utilized microarray.

32. The method of claim 8 wherein the mapping step utilizes fractal filtering to map the identified hybridization activity to coordinates on the viral diffusion curve.

33. The method of claim 8 wherein the generation step employs nonlinear information filtering.

DISCUSSION

In response to the Final Office Action dated April 5, 2002, Applicant has deleted claims 6-7; 9-25 which were previously withdrawn from consideration by the Examiner, and respectfully requests entry and consideration of amended claim 8, and new claims 26-33 directed towards the elected invention, namely a technique for determining viral load from a patient via use of a viral diffusion curve determined from a microarray output.

With regard to the double patenting and enablement rejections of claim 8, Applicant has amended the claim from a computer system accomplishing a method to a method claim. Amended claim 8 covers a method for quantitating viral load using to measurements without reference to known viral load studies. This is similar in scope to, *inter alia*, system claims 19 and 46 which do not require known viral load studies to construct a viral diffusion curve, but simply require two or more viral load measurements.

The amended claim 8, while having similar breadth to several apparatus claims in the '511 patent, is not coextensive in scope to claim 34 of the '511 patent as it has been amended

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from an apparatus claim to a method claim. In addition, Applicant believes that amended claim 8 is also not coextensive with any of the other method claims within the '511 patent as claims 1 and 14 of the '511 patent are directed, *inter alia*, to the generation of a viral diffusion curve "based on known viral load studies", whereas amended claim 8 covers a system that can generate a viral diffusion curve based on two measurements without reference to known viral load studies, and claims 41, 42, and 45 of the '511 patent are of sufficiently different scope than the current amended claim 8. For example, claims 41 and 42 are in some aspects broader than amended claim 8 as they both relate to viral load measurements using biochip output patterns to measure viral and to determine if a therapy was effective. Moreover, claim 45 relates to a method for determining the effectiveness of a therapy that includes the generation of a viral diffusion curve which may or not relate to known viral load studies, the mapping of the output patterns to the viral diffusion curve using fractal filtering (amended claim 8 does not include the step of fractal filtering), the determination of convergence (amended claim 8 does not include this step), and determining if the therapy was effective (amended claim 8 does not include this step). Accordingly, because claim 8 has been amended to a method claim and has a different scope than all of the claims within the '511 patent, Applicant respectfully requests that the double patenting rejection be withdrawn.

Support for the determination of viral load using two measurements within amended claim 8 can be found within the following passages:

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Excerpt from Page 27, line 6 – Page 29, line 6:

The VDC representation models a stochastic process given by

$$W(f)(x,y)=\begin{cases}\gamma_i \cdot f\left(\frac{1}{\sigma_i}\left(\frac{x-x_D^i}{y-y_D^i}\right)+\frac{x_R^i}{y_R^i}\right)+\tau\left(\frac{x-x_D^i}{y-y_D^i}\right)+\beta_i, \\ \qquad if(x,y) \in \mu_i^{-1}(1), \text{for some } 1\le i\le m; \\ 0, \qquad otherwise;\end{cases}$$

for any $(x,y)\in\Re^2$ and $f \in \wp(\Re^2)$

An exemplary partitioned iterated fractal system (IFS) model for the system is

$$W=\{\Phi_i=(\mu_i,T_i)\}i=1,2,...,m$$

where the affine parameters for the IFS transformation are given by

$$T_i=\left((x_D^i,y_D^i),(x_R^i,y_R^i),\ \sigma_i=\begin{pmatrix}s_{00}^i & s_{01}^i\\ s_{10}^i & s_{11}^i\end{pmatrix},\tau_i=(t_0^i,t_1^i),\gamma_i,\beta_i\right)$$

where the D - origin is given by (x_D^i, y_D^i),
the R - origin is given by (x_R^i, y_R^i)
spatial transformation matrix is given by σ_i
the intensity tilting vector is given by τ_i
the contrast adjuctment is given by γ_i
the brightness adjustment is given by β_i

and wherein Φ represents the enhanced dot spectrogram and wherein μ represents the calculated expectation match values

This IFS model maps the dot spectrogram to a point on the VDC wherein each VDC coordinate is denoted by VDC(t,Θ) such that

$W[\Phi, k] \rightarrow VDC(k, \Theta)$

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